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PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/701,572

DATE: 07/27/2001
 TIME: 19:50:19

Input Set : A:\ES.txt
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ENTERED

3 <110> APPLICANT: KONDOROSI, Eva
 4 CEBOLLA, Angel
 5 KONDOROSI, Adam
 7 <120> TITLE OF INVENTION: PLANT PROTEIN WITH REPEATED WD40 MOTIFFS, NUCLEIC ACID
 CODING FOR SAID

8 PROTEIN, AND USES THEREOF
 10 <130> FILE REFERENCE: 200204US0PCT
 12 <140> CURRENT APPLICATION NUMBER: 09/701,572
 13 <141> CURRENT FILING DATE: 2000-12-08
 15 <150> PRIOR APPLICATION NUMBER: PCT/FR99/01`342
 16 <151> PRIOR FILING DATE: 1999-06-08
 18 <150> PRIOR APPLICATION NUMBER: FR07174
 19 <151> PRIOR FILING DATE: 1998-08-06
 21 <160> NUMBER OF SEQ ID NOS: 13
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2006
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Medicago sativa
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (182)..(1609)
 33 <223> OTHER INFORMATION:
 36 <400> SEQUENCE: 1
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 39 ttttcgagta gtgtatttt ttaataaaaa attaatattt tttttttat ataaaagccg 120
 41 tgcaaaaaat tcttttacag cgttcttttt tcccgggaa aaaaattaac acagctccgc 180
 43 c atg gac gga acc ggt aat cga aat cca cca ccg act tcc acc gtc aga 229
 44 Met Asp Gly Thr Gly Asn Arg Asn Pro Pro Pro Thr Ser Thr Val Arg
 45 1 5 10 15
 47 gac aat tct cca ccg cct gag cca tca ccg gag agt ctc cgt cat gta 277
 48 Asp Asn Ser Pro Pro Pro Glu Pro Ser Pro Glu Ser Leu Arg His Val
 49 20 25 30
 51 agc cgt atg atc aac agc aac cat tac acc tca cct tct cga aca atc 325
 52 Ser Arg Met Ile Asn Ser Asn His Tyr Thr Ser Pro Ser Arg Thr Ile
 53 35 40 45
 55 tac tcc gat agg ttc att ccg agt aga tct gct tcg aaa ttc gct ttg 373
 56 Tyr Ser Asp Arg Phe Ile Pro Ser Arg Ser Ala Ser Lys Phe Ala Leu
 57 50 55 60
 59 ttt gat atc aat act ccg aca gaa gga cgc gat gat agt tcc agc gct 421
 60 Phe Asp Ile Asn Thr Pro Thr Glu Gly Arg Asp Asp Ser Ser Ser Ala
 61 65 70 75 80
 63 tat acg act ctt ctg aga acg gcg ttg ttt gga ccg gat gtt gcc ggt 469
 64 Tyr Thr Thr Leu Leu Arg Thr Ala Leu Phe Gly Pro Asp Val Ala Gly
 65 85 90 95
 67 ccg gtt acg ccg gaa aaa acc gac tcg ccg tcg atg aca ttg ccg aat 517
 68 Pro Val Thr Pro Glu Lys Thr Asp Ser Pro Ser Met Thr Leu Pro Asn
 69 100 105 110

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71	agg aat att ttt agg tat aag acg gag acg aga cag tcc atg cac tcg	565
72	Arg Asn Ile Phe Arg Tyr Lys Thr Glu Thr Arg Gln Ser Met His Ser	
73	115 120 125	
75	ctt tcg ccg ttt atg gat gat ttt gtt cct ggt gtt aat cat agt	613
76	Leu Ser Pro Phe Met Asp Asp Phe Val Pro Gly Val Asn His Ser	
77	130 135 140	
79	ccg gtt aag gct cct agg aag gtt cct cga tcg cct tat aag gtt ttg	661
80	Pro Val Lys Ala Pro Arg Lys Val Pro Arg Ser Pro Tyr Lys Val Leu	
81	145 150 155 160	
83	gat gca cct gct ttg caa gat gat ttt tat ctg aat ctg gta gat tgg	709
84	Asp Ala Pro Ala Leu Gln Asp Asp Phe Tyr Leu Asn Leu Val Asp Trp	
85	165 170 175	
87	tct tca cac aat gtg ttg gct gtt ggt ttg ggt aac tgt gtc tat ctc	757
88	Ser Ser His Asn Val Leu Ala Val Gly Leu Gly Asn Cys Val Tyr Leu	
89	180 185 190	
91	tgg aat gct tgt agc agc aag gta act aaa tta tgt gat ttg ggg gtt	805
92	Trp Asn Ala Cys Ser Ser Lys Val Thr Lys Leu Cys Asp Leu Gly Val	
93	195 200 205	
95	gat gat tgt gtt tgt tct gtt ggt tgg gct caa cgt ggt act cat ctt	853
96	Asp Asp Cys Val Cys Ser Val Gly Trp Ala Gln Arg Gly Thr His Leu	
97	210 215 220	
99	gct gtt gga act aac aat ggt aaa gtt cag att tgg gat gca gca aga	901
100	Ala Val Gly Thr Asn Asn Gly Lys Val Gln Ile Trp Asp Ala Ala Arg	
101	225 230 235 240	
103	tgc aag aag ata aga tca atg gag ggc cat cgg tta cgt gtc ggg gcc	949
104	Cys Lys Lys Ile Arg Ser Met Glu Gly His Arg Leu Arg Val Gly Ala	
105	245 250 255	
107	ttg gcc tgg agt tca tct ctt ttg tct tct ggt gga cgg gat aag aat	997
108	Leu Ala Trp Ser Ser Ser Leu Leu Ser Ser Gly Gly Arg Asp Lys Asn	
109	260 265 270	
111	att tat caa cga gat ata cgc aca caa gaa gat ttt gtt agt aaa ctg	1045
112	Ile Tyr Gln Arg Asp Ile Arg Thr Gln Glu Asp Phe Val Ser Lys Leu	
113	275 280 285	
115	tca gga cac aaa tca gag gtt tgt gga ctg aag tgg tca tat gat aac	1093
116	Ser Gly His Lys Ser Glu Val Cys Gly Leu Lys Trp Ser Tyr Asp Asn	
117	290 295 300	
119	cgt gag ttg gca tct gga gga aat gac aac aaa ttg ttt gtt tgg aat	1141
120	Arg Glu Leu Ala Ser Gly Gly Asn Asp Asn Lys Leu Phe Val Trp Asn	
121	305 310 315 320	
123	caa cac tca acc cag cct gtc ctc aag tac tgt gag cac aca gca gct	1189
124	Gln His Ser Thr Gln Pro Val Leu Lys Tyr Cys Glu His Thr Ala Ala	
125	325 330 335	
127	gtt aaa gct att gca tgg tct cct cat ctt cat gga ctt ctt gca tct	1237
128	Val Lys Ala Ile Ala Trp Ser Pro His Leu His Gly Leu Leu Ala Ser	
129	340 345 350	
131	gga gga gga act gca gat aga tgt att cgt ttt tgg aat aca acc aca	1285
132	Gly Gly Gly Thr Ala Asp Arg Cys Ile Arg Phe Trp Asn Thr Thr Thr	
133	355 360 365	
135	aac tca cac ctt agc tgt atg gac act gga agt cag gtt tgc aat ctt	1333

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136 Asn Ser His Leu Ser Cys Met Asp Thr Gly Ser Gln Val Cys Asn Leu
137      370      375      380
139 gtc tgg tcc aaa aat gtc aac gaa cta gta agc aca cat ggg tac tcc      1381
140 Val Trp Ser Lys Asn Val Asn Glu Leu Val Ser Thr His Gly Tyr Ser
141 385      390      395      400
143 cag aac cag att att gtt tgg aga tac ccc act atg tca aag ctg gcg      1429
144 Gln Asn Gln Ile Ile Val Trp Arg Tyr Pro Thr Met Ser Lys Leu Ala
145      405      410      415
147 act ctt acc ggc cat act tat agg gtt ctc tat ctt gcc atc tct cca      1477
148 Thr Leu Thr Gly His Thr Tyr Arg Val Leu Tyr Leu Ala Ile Ser Pro
149      420      425      430
151 gat gga cag act att gta act gga gct gga gat gaa acg ctt agg ttc      1525
152 Asp Gly Gln Thr Ile Val Thr Gly Ala Gly Asp Glu Thr Leu Arg Phe
153      435      440      445
155 tgg aat gtt ttc cct tcc cct aaa tca cag aat act gaa agt gaa atc      1573
156 Trp Asn Val Phe Pro Ser Pro Lys Ser Gln Asn Thr Glu Ser Glu Ile
157      450      455      460
159 gga gca tta tct ctt gga aga act act atc agg tga ttgatcctgg      1619
160 Gly Ala Leu Ser Leu Gly Arg Thr Thr Ile Arg
161 465      470      475
163 cggtgcagcc caatcatgtg gcatatttct aagtttgggt tgctgtgtag aactaaattt      1679
165 ctgagcggag aacaccatgg tggaaaaacc ttgaatataa aaacaccacc aaagtagcat      1739
167 ctttaccacac tgggagagcc ttggagggag ctataaaagt tttgatatgg ctgccggtga      1799
169 tattcctgca ttcattgtgta gtctcatttt atattgaaaa gatgataaca aatgggtaat      1859
171 ttattgtctt ggacttatac atgcattgat ggagttgtag ccaagttttt ttattactct      1919
173 ttttttcttt cttctttttg atagtgtctt cctgcattat ttatataatt ttaagatgcg      1979
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183 <400> SEQUENCE: 2
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186 1      5      10      15
189 Asp Asn Ser Pro Pro Pro Glu Pro Ser Pro Glu Ser Leu Arg His Val
190      20      25      30
193 Ser Arg Met Ile Asn Ser Asn His Tyr Thr Ser Pro Ser Arg Thr Ile
194      35      40      45
197 Tyr Ser Asp Arg Phe Ile Pro Ser Arg Ser Ala Ser Lys Phe Ala Leu
198      50      55      60
201 Phe Asp Ile Asn Thr Pro Thr Glu Gly Arg Asp Asp Ser Ser Ser Ala
202 65      70      75      80
205 Tyr Thr Thr Leu Leu Arg Thr Ala Leu Phe Gly Pro Asp Val Ala Gly
206      85      90      95
209 Pro Val Thr Pro Glu Lys Thr Asp Ser Pro Ser Met Thr Leu Pro Asn
210      100      105      110
213 Arg Asn Ile Phe Arg Tyr Lys Thr Glu Thr Arg Gln Ser Met His Ser
214      115      120      125
217 Leu Ser Pro Phe Met Asp Asp Asp Phe Val Pro Gly Val Asn His Ser

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218      130      135      140
221 Pro Val Lys Ala Pro Arg Lys Val Pro Arg Ser Pro Tyr Lys Val Leu
222 145      150      155      160
225 Asp Ala Pro Ala Leu Gln Asp Asp Phe Tyr Leu Asn Leu Val Asp Trp
226      165      170      175
229 Ser Ser His Asn Val Leu Ala Val Gly Leu Gly Asn Cys Val Tyr Leu
230      180      185      190
233 Trp Asn Ala Cys Ser Ser Lys Val Thr Lys Leu Cys Asp Leu Gly Val
234      195      200      205
237 Asp Asp Cys Val Cys Ser Val Gly Trp Ala Gln Arg Gly Thr His Leu
238      210      215      220
241 Ala Val Gly Thr Asn Asn Gly Lys Val Gln Ile Trp Asp Ala Ala Arg
242 225      230      235      240
245 Cys Lys Lys Ile Arg Ser Met Glu Gly His Arg Leu Arg Val Gly Ala
246      245      250      255
249 Leu Ala Trp Ser Ser Ser Leu Leu Ser Ser Gly Gly Arg Asp Lys Asn
250      260      265      270
253 Ile Tyr Gln Arg Asp Ile Arg Thr Gln Glu Asp Phe Val Ser Lys Leu
254      275      280      285
257 Ser Gly His Lys Ser Glu Val Cys Gly Leu Lys Trp Ser Tyr Asp Asn
258      290      295      300
261 Arg Glu Leu Ala Ser Gly Gly Asn Asp Asn Lys Leu Phe Val Trp Asn
262 305      310      315      320
265 Gln His Ser Thr Gln Pro Val Leu Lys Tyr Cys Glu His Thr Ala Ala
266      325      330      335
269 Val Lys Ala Ile Ala Trp Ser Pro His Leu His Gly Leu Leu Ala Ser
270      340      345      350
273 Gly Gly Gly Thr Ala Asp Arg Cys Ile Arg Phe Trp Asn Thr Thr Thr
274      355      360      365
277 Asn Ser His Leu Ser Cys Met Asp Thr Gly Ser Gln Val Cys Asn Leu
278      370      375      380
281 Val Trp Ser Lys Asn Val Asn Glu Leu Val Ser Thr His Gly Tyr Ser
282 385      390      395      400
285 Gln Asn Gln Ile Ile Val Trp Arg Tyr Pro Thr Met Ser Lys Leu Ala
286      405      410      415
289 Thr Leu Thr Gly His Thr Tyr Arg Val Leu Tyr Leu Ala Ile Ser Pro
290      420      425      430
293 Asp Gly Gln Thr Ile Val Thr Gly Ala Gly Asp Glu Thr Leu Arg Phe
294      435      440      445
297 Trp Asn Val Phe Pro Ser Pro Lys Ser Gln Asn Thr Glu Ser Glu Ile
298      450      455      460
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302 465      470      475
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306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: synthetic DNA

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313 <400> SEQUENCE: 3
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319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: synthetic DNA
325 <400> SEQUENCE: 4
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329 <210> SEQ ID NO: 5
330 <211> LENGTH: 25
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: synthetic DNA
337 <400> SEQUENCE: 5
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341 <210> SEQ ID NO: 6
342 <211> LENGTH: 56
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: synthetic DNA
349 <400> SEQUENCE: 6
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353 <210> SEQ ID NO: 7
354 <211> LENGTH: 526
355 <212> TYPE: PRT
356 <213> ORGANISM: Drosophila melanogaster
358 <400> SEQUENCE: 7
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364 Asp Gly Glu Thr Arg Gly Pro Ala Pro Arg Trp Lys Lys Lys Leu Glu
365 20 25 30
368 Ala Ser Leu Asn Gly Ser Val Asn Thr Thr Arg Ser Val Leu Ser Val
369 35 40 45
372 Ser Tyr Asn Thr Ser Phe Ser Gly Val Gln Ala Pro Thr Lys Thr Pro
373 50 55 60
376 Gly Lys Ser Ser Glu Gly Lys Thr Lys Lys Ser Asn Thr Thr Pro Ser
377 65 70 75 80
380 Lys Thr Pro Gly Gly Asp Arg Phe Ile Pro Asn Arg Ala Ala Thr
381 85 90 95
384 Asn Phe Glu Leu Ala His Phe Leu Val Asn Lys Asp Ser Gly Asp Lys
385 100 105 110
388 Ser Asp Glu Glu Asn Asp Lys Ala Thr Ser Ser Asn Ser Asn Glu Ser
389 115 120 125
392 Asn Val Gln Ala Ser Ala His Lys Gly Asp Arg Gln Lys Leu Ile Ser
393 130 135 140

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VERIFICATION SUMMARY

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